

Dietmar Spengler and Laurent Journot  
Serial No.: 09/254,870  
Filed: August 16, 1999  
Page 2

comply with the Sequence Rules and that applicants must provide  
1) a substitute computer readable form (CRF) copy of the  
"Sequence Listing"; 2) a substitute paper copy of the "Sequence  
Listing ", as well as an amendment directing its entry into the  
specification; AND 3) a statement that the content of the paper  
and computer readable copies are the same and, where applicable,  
include no new matter, as required by 37 C.F.R. §1.821(e) or  
§1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

Please amend the specification as follows:

In the Specification

Please delete the previously submitted paper copy of the  
"Sequence Listing" inserted after page 71.

Please insert after page 71 the amended paper copy of the  
"Sequence Listing", attached to hereto as **Exhibit B**.

REMARKS

In response to the May 24, 2000 Notice, applicants submit  
herewith a computer readable form (CRF) copy of a revised  
Sequence Listing which is set forth on the newly submitted paper  
copy of revised Sequence Listing.

Applicants further submit a paper copy of the revised Sequence  
Listing, attached hereto as **Exhibit B**, and a Statement in  
Accordance with 37 C.F.R. §1.821(f), attached hereto as **Exhibit  
C**, certifying that the computer readable form as required by 37  
C.F.R. §1.821(e) is identical to the paper copy of Sequence

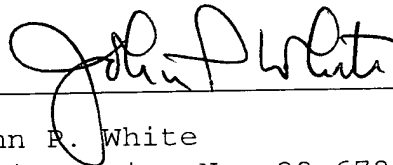
Dietmar Spengler and Laurent Journot  
Serial No.: 09/254,870  
Filed: August 16, 1999  
Page 3

Listing.

Applicants are submitting herewith a computer diskette containing a C.F.R. of the sequence listing.

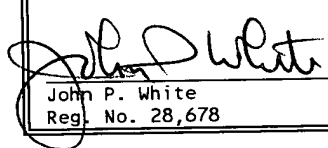
No fee is deemed necessary in connection with the filing of this Amendment. However, if any fee is required, authorization is hereby given to charge the amount of any such fee to Deposit Account No. 03-3125.

Respectfully submitted,



John P. White  
Registration No. 28,678  
Attorney for Applicants  
Cooper & Dunham LLP  
1185 Avenue of the Americas  
New York, New York 10036  
(212) 278-0400

I hereby certify that this correspondence is being deposited this date with the U.S. Postal Service with sufficient postage as first class mail addressed to: Assistant Commissioner for Patents and Trademarks, Washington, D.C. 20231.



John P. White  
Reg. No. 28,678

Date

6/26/00



UNITED STATES DEPARTMENT OF COMMERCE  
Patent Trademark Office  
COMMISSIONER OF PATENTS AND  
TRADEMARKS  
Washington, D.C. 20231 JPW  
52/30-A-PCT-US

DEA/FCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER
	7

DATE MAILED: 5/24/00

1mo: 6/24/00

6mo: 11/24/00 W.D.

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents  
This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 because applicant has not submitted a CRF.

APPLICANT IS GIVEN ONE MONTH, or THIRTY DAYS, WHICHEVER IS LONGER FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for response beyond the SIX MONTH statutory period. Direct the response to the undersigned.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Charles L. Patterson, Jr., Ph.D. whose telephone number is (703) 308-1834. The examiner can normally be reached on any day of the week from 7:30 AM until 4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy, can be reached on (703) 308-3804. The fax phone number for this Group is (703) 305-7401.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Patterson  
May 18, 2000

CHARLES L. PATTERSON, JR.  
PRIMARY EXAMINER  
GROUP 1800



## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

#### (i) APPLICANT:

- (A) NAME: Max-Planck-Gesellschaft zur Foerderung der  
Wissenschaften e.V.  
(B) STREET: none  
(C) CITY: Berlin  
(E) COUNTRY: DE  
(F) POSTAL CODE (ZIP): none

- (A) NAME: CNRS  
(B) STREET: rue de la cardonille  
(C) CITY: Montpellier Cedex 05  
(E) COUNTRY: FR  
(F) POSTAL CODE (ZIP): 34094

(ii) TITLE OF INVENTION: Nucleic acid molecules coding for mammalian  
tumor suppressor proteins and methods for their isolation

(iii) NUMBER OF SEQUENCES: 17

#### (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

### (2) INFORMATION FOR SEQ ID NO: 1:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2790 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

#### (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 542..2545

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCGGGA GAGCAAGCGG GCATCTCCTG GGCGCCGTCA TGGCTGCTTA GGCTGCGCTG 60  
CCTGCGGATC GCGGATCCGG GATCGGAGAT CTGACGGCGA CGCCTGAGTC CGGCTAGGGT 120  
AGGTCTGGGT TGGAGTCTGT GCCTGCTTCC TTGGCGTGTG GTTGTTCTCTG CTTGATTGCT 180  
TCAGCGTGCC ATCGGCTTCG TATTTGCATA GGAGTCAGAG GAGTTAATCT TGTCTCCTCG 240  
AAGATAGACT CTCATGGTTT ATGATCCATC TCTGTGAGAA GACTTTATTT GTCTGTCTCT 300

TCTCACAGGT TTGAGTCTTC AGACTTCTAC AGAACTCCAT AATATCTGCC TCACAGCTGG	360
CTTTCCTGCT CTCACAGAAG ATACCCAGCT ATTGTGCTCT GGATCTCTCC TGGCTGCTAG	420
GCTGTAGCGC TGCCTTTCTG GAGTCAGGCT GTAGTGACTC CCCACCTTCT TTCTGTCTGG	480
GCTTAAATGG CACAGCAGTT CCTCAGCACA TCTGAAGAAG AAAGTGTGAG AACCAAAGGC	540
C ATG GCT CCA TTC CGC TGT CAA AAA TGT GGC AAG TCC TTC GTC ACC	586
Met Ala Pro Phe Arg Cys Gln Lys Cys Gly Lys Ser Phe Val Thr	
1 5 10 15	
CTG GAG AAG TTC ACC ATT CAC AAT TAT TCC CAC TCC AGG GAG CGC CCA	634
Leu Glu Lys Phe Thr Ile His Asn Tyr Ser His Ser Arg Glu Arg Pro	
20 25 30	
TTC AAG TGC TCG AAG GCT GAG TGT GGC AAA GCC TTC GTC TCC AAG TAT	682
Phe Lys Cys Ser Lys Ala Glu Cys Gly Lys Ala Phe Val Ser Lys Tyr	
35 40 45	
AAG CTG ATG AGA CAC ATG GCC ACA CAC TCG CCA CAG AAG ATT CAC CAG	730
Lys Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ile His Gln	
50 55 60	
TGT ACT CAC TGT GAG AAG ACA TTC AAC CGG AAG GAC CAC CTG AAG AAC	778
Cys Thr His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys Asn	
65 70 75	
CAC CTC CAG ACC CAC GAT CCC AAC AAG ATC TCC TAC GCG TGT GAC GAT	826
His Leu Gln Thr His Asp Pro Asn Lys Ile Ser Tyr Ala Cys Asp Asp	
80 85 90 95	
TGC GGC AAG AAG TAC CAC ACC ATG CTG GGC TAC AAG AGG CAC CTG GCC	874
Cys Gly Lys Lys Tyr His Thr Met Leu Gly Tyr Lys Arg His Leu Ala	
100 105 110	
CTG CAC TCG GCG AGC AAT GGC GAT CTC ACC TGT GGG GTG TGC ACC CTG	922
Leu His Ser Ala Ser Asn Gly Asp Leu Thr Cys Gly Val Cys Thr Leu	
115 120 125	
GAG CTG GGG AGC ACC GAG GTC CTG CTG GAC CAC CTC AAG TCT CAC GCG	970
Glu Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ser His Ala	
130 135 140	
GAA GAA AAG GCC AAC CAG GCA CCC AGG GAG AAG AAA TAC CAG TGC GAC	1018
Glu Glu Lys Ala Asn Gln Ala Pro Arg Glu Lys Lys Tyr Gln Cys Asp	
145 150 155	
CAC TGT GAT AGA TGC TTC TAC ACC CGG AAA GAT GTG CGT CGC CAC CTG	1066
His Cys Asp Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg-His Leu	
160 165 170 175	
GTG GTC CAC ACA GGA TGC AAG GAC TTC CTG TGT CAG TTC TGT GCC CAG	1114
Val Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln	
180 185 190	
AGA TTT GGG CGC AAA GAC CAC CTC ACT CGT CAC ACC AAG AAG ACC CAC	1162
Arg Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His	
195 200 205	

TCC CAG GAG CTG ATG CAA GAG AAT ATG CAG GCA GGA GAT TAC CAG AGC Ser Gln Glu Leu Met Gln Glu Asn Met Gln Ala Gly Asp Tyr Gln Ser 210 215 220	1210
AAT TTC CAA CTC ATT GCG CCT TCA ACT TCG TTC CAG ATA AAG GTT GAT Asn Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp 225 230 235	1258
CCC ATG CCT CCT TTC CAG CTA GGA GCG GCT CCC GAG AAC GGG CTT GAT Pro Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu Asp 240 245 250 255	1306
GGT GGC TTG CCA CCC GAG GTT CAT GGT CTA GTG CTT GCT GCC CCA GAA Gly Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro Glu 260 265 270	1354
GAA GCT CCC CAA CCC ATG CCG CCC TTG GAG CCT TTG GAG CCT TTG GAG Glu Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu 275 280 285	1402
CCT TTG GAG CCT TTG GAG CCG ATG CAG TCT TTG GAG CCT TTG CAG CCT Pro Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln Pro 290 295 300	1450
TTG GAG CCG ATG CAG CCT TTG GAG CCA ATG CAG CCT TTG GAG CCG ATG Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met 305 310 315	1498
CAG CCT TTA GAG CCT TTG GAG CCT CTG GAG CCG ATG CAG CCT TTG GAG Gln Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu Glu 320 325 330 335	1546
CCG ATG CAG CCT TTG GAG CCT ATG CAG CCA ATG CTG CCA ATG CAG CCA Pro Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln Pro 340 345 350	1594
ATG CAG CCA ATG CAG CCA ATG CAG CCA ATG CTG CCA ATG CAG CCA ATG Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro Met 355 360 365	1642
CTG CCA ATG CAG CCA ATG CAG CCA ATG CAG CCA ATG CTG CCA ATG CCA Leu Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Pro 370 375 380	1690
GAG CCG TCT TTC ACT CTG CAC CCT GGC GTA GTT CCC ACC TCT CCT CCC Glu Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro Pro 385 390 395	1738
CCA ATT ATT CTT CAG GAG CAT AAG TAT AAT CCT GTT CCT ACC TCA TAT Pro Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser Tyr 400 405 410 415	1786
GCC CCA TTT GTA GGC ATG CCC GTC AAA GCA GAT GGC AAG GCC TTT TGC Ala Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe Cys 420 425 430	1834
AAC GTG GGT TTC TTT GAG GAA TTT CCT CTG CAA GAG CCT CAG GCG CCT Asn Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala Pro	1882

435	440	445	
CTC AAG TTC AAC CCA TGT TTT GAG ATG CCT ATG GAG GGG TTT GGG AAA Leu Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly Lys 450 455 460			1930
GTC ACC CTG TCC AAA GAG CTG CTG GTA GAT GCT GTG AAT ATA GCC ATT Val Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile 465 470 475			1978
CCT GCC TCT CTG GAG ATT TCC TCC CTA TTG GGG TTT TGG CAG CTC CCC Pro Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro 480 485 490 495			2026
CCT CCT ACT CCC CAG AAT GGC TTT GTG AAT AGC ACC ATC CCT GTG GGG Pro Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly 500 505 510			2074
CCT GGG GAG CCA CTG CCC CAT AGG ATA ACC TGT CTG GCG CAG CAG CAG Pro Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln Gln 515 520 525			2122
CCA CCG CCA CTG CCG CCG CCA CCA CCG CTG CCA CTG CCA CAG CCA CTG Pro Pro Pro Leu Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu 530 535 540			2170
CCA GTG CCA CAG CCA CTA CCA CAG CCA CAG ATG CAG CCA CAG TTT CAG Pro Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln 545 550 555			2218
TTG CAG ATC CAG CCC CAG ATG CAG CTA CCA CAG CTG CTG CCG CAA CTG Leu Gln Ile Gln Pro Gln Met Gln Leu Pro Gln Leu Leu Pro Gln Leu 560 565 570 575			2266
CAA CCT CAG CAG CAG COT GAT CCT GAG CCA GAG CCA GAG CCA GAG CCA Gln Pro Gln Gln Gln Pro Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro 580 585 590			2314
GAG CCA GAG CCA GAG CCA GAG CCG GAA CCG GAA CCG GAG CCA GAG CCA Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro 595 600 605			2362
GAG CCA GAA CCA GAG CCA GAG GAA GAA CAG GAA GAG GCA GAA GAA GAG Glu Pro Glu Pro Glu Pro Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu 610 615 620			2410
GCA GAG GAA GGA GCA GAG GAA GGA GCA GAA CCA GAG GCA CAG GCA GAA Ala Glu Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu 625 630 635			2458
GAA GAG GAA GAG GAA GAG GAA GCG GAA GAG CCA CAG CCA GAA GAA GCC Glu Glu Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala 640 645 650 655			2506
CAA ATA GCA GGA CTC GTC TAT AAG AAA TGG ACA GTT TAG TTCCTCTTCT Gln Ile Ala Gly Leu Val Tyr Lys Lys Trp Thr Val 660 665			2555
TGTTAGCTTA CTCTGTAGTT TCTTCTTCTT GTTGCCCATTT GTGTAGCTTT ATAGAGTGTG			2615

ACGCTATTGA TGTCTCCATT TTTTAAAGTG AATTTAAATG TACTGTTCAA TATTTTTCAT	2675
GTGATGTTGT TCCAATGTGA GTTACGACTT CATTTATCTT AAAGACAAA CTGGTTGTCA	2735
GTCATATCTG ACAGAAGAAA GAAATCACTG TGTAACCAAG CCATATAGCG GCCGC	2790

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 668 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Pro	Phe	Arg	Cys	Gln	Lys	Cys	Gly	Lys	Ser	Phe	Val	Thr	Leu	1	5	10	15
Glu	Lys	Phe	Thr	Ile	His	Asn	Tyr	Ser	His	Ser	Arg	Glu	Arg	Pro	Phe	20	25	30	
Lys	Cys	Ser	Lys	Ala	Glu	Cys	Gly	Lys	Ala	Phe	Val	Ser	Lys	Tyr	Lys	35	40	45	
Leu	Met	Arg	His	Met	Ala	Thr	His	Ser	Pro	Gln	Lys	Ile	His	Gln	Cys	50	55	60	
Thr	His	Cys	Glu	Lys	Thr	Phe	Asn	Arg	Lys	Asp	His	Leu	Lys	Asn	His	65	70	75	80
Leu	Gln	Thr	His	Asp	Pro	Asn	Lys	Ile	Ser	Tyr	Ala	Cys	Asp	Asp	Cys	85	90	95	
Gly	Lys	Lys	Tyr	His	Thr	Met	Leu	Gly	Tyr	Lys	Arg	His	Leu	Ala	Leu	100	105	110	
His	Ser	Ala	Ser	Asn	Gly	Asp	Leu	Thr	Cys	Gly	Val	Cys	Thr	Leu	Glu	115	120	125	
Leu	Gly	Ser	Thr	Glu	Val	Leu	Leu	Asp	His	Leu	Lys	Ser	His	Ala	Glu	130	135	140	
Glu	Lys	Ala	Asn	Gln	Ala	Pro	Arg	Glu	Lys	Lys	Tyr	Gln	Cys	Asp	His	145	150	155	160
Cys	Asp	Arg	Cys	Phe	Tyr	Thr	Arg	Lys	Asp	Val	Arg	Arg	His	Leu	Val	165	170	175	
Val	His	Thr	Gly	Cys	Lys	Asp	Phe	Leu	Cys	Gln	Phe	Cys	Ala	Gln	Arg	180	185	190	
Phe	Gly	Arg	Lys	Asp	His	Leu	Thr	Arg	His	Thr	Lys	Lys	Thr	His	Ser	195	200	205	
Gln	Glu	Leu	Met	Gln	Glu	Asn	Met	Gln	Ala	Gly	Asp	Tyr	Gln	Ser	Asn				



210	215	220
Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp Pro		
225	230	235 240
Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu Asp Gly		
	245	250 255
Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro Glu Glu		
	260	265 270
Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro		
	275	280 285
Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln Pro Leu		
	290	295 300
Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln		
305	310	315 320
Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu Glu Pro		
	325	330 335
Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln Pro Met		
	340	345 350
Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro Met Leu		
	355	360 365
Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Pro Glu		
	370	375 380
Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro Pro Pro		
385	390	395 400
Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser Tyr Ala		
	405	410 415
Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe Cys Asn		
	420	425 430
Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala Pro Leu		
	435	440 445
Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly Lys Val		
	450	455 460
Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile Pro		
465	470	475 480
Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro Pro		
	485	490 495
Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly Pro		
	500	505 510
Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln Gln Pro		
	515	520 525

Pro Pro Leu Pro Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu Pro  
 530 535 540  
 Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln Leu  
 545 550 555 560  
 Gln Ile Gln Pro Gln Met Gln Leu Pro Gln Leu Leu Pro Gln Leu Gln  
 565 570 575  
 Pro Gln Gln Gln Pro Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu  
 580 585 590  
 Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu  
 595 600 605  
 Pro Glu Pro Glu Pro Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu Ala  
 610 615 620  
 Glu Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu Glu  
 625 630 635 640  
 Glu Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala Gln  
 645 650 655  
 Ile Ala Gly Leu Val Tyr Lys Lys Trp Thr Val \*  
 660 665

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGTCTCGAG GCCTTTGCGG CCGCTATANN NNNNNN

36

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGCCATGG

9

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "N at position 3 is A or G."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCNCCATGG

9

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

His Ser Arg Glu Arg Pro Phe Lys Cys  
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Cross-links
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "X at position 2 is S or T."

(ix) FEATURE:

- (A) NAME/KEY: Cross-links
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "X at position 7 is F or Y."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

His Xaa Gly Glu Lys Pro Xaa Xaa Cys  
1 5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

His Ser Pro Gln Lys  
1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Lys Lys Trp Thr  
1

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTGATGGCGG CCGCCATTCC GCTGTCAAAA ATGTG

35

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCGCGCCTCG AGGGTCTTCT TGGTGTGACG

30

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCGGCCGCAG AGCCGTCTTT CACTC

25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCGCGCCTCG AGAACTGTCC ATTTCTTATA GAC

33

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATAGCAGTGA GTGCTGTG

18

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GTTTCTTTTC AGGGACTC

18

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2334 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 803..2192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CGGTTCTTTC AATTCAGAAT TTGTTTTAGG TTCTGTTATT GCATAGATTT GCATACCTGT	60
TTTATGGTAT TTTAATACTG TTGGTTTTAA AAAATACCAT TTCCTCTGAG TGCTGTTCTG	120
AATATATTAT GTAAGCAATT TTGTGTGTTT TTTTTTTTCC ACTTGCATAA AGCAGGGGAA	180
AAGTTGAGAG TTTTCTTAA TCCAGTCCCA AGTAGGACAA AGGATATGAG TGTTTAAAGA	240
TCATCTATTA AAATGCATGA AAAAACTA GAAATCTCC TGTGCACATC GCCAGTCGTG	300
TGTGTGCTCT AGAAGTGAAG TTCAGGGGGT AACATAATGG AGGAATGTTT TCCTAGCTTC	360
ATTCCCTGAC GATGTACAAG GTCTCTTCTC ACAGGTTTGA ATCTTCAGAC AAACCTCTGG	420

GAGGACTGGG AGGACTCGGT CCCTGCCTCG CAGCAGATGT TCCCTGTCAC TCAGTAGCCA	480
ATCCGGGGGA CCCAGGACAT GCCCCAGCTA TAGTGATGCA GATTACCTTT CTGGTCCTGA	540
ATCGCACCTG TGCCTCGAGA CTTTCTCCCC TCAGCTTGAG ACTGCATGTA AACTGGGATG	600
TGTGAAAGCA GGAAGCAAAG CTAGTGACAG CTGAGAGGTC CATGTCTGGG TAGAACCAGG	660
CCCACGATGC TGCCTCTCCC GTGGTCTGGA GTTCAGCTGC AGGGACTCTG CTGATTGGCC	720
CAGCACCATC GTTCTGTTTG TGCTTAAATG GCACAGCATT TGGTCAGCAC ATCTGAAAAG	780
GAAGGTGTGA GAAGCAAAGC CC ATG GCC ACG TTC CCC TGC CAG TTA TGT GGC	832
Met Ala Thr Phe Pro Cys Gln Leu Cys Gly	
1 5 10	
AAG ACG TTC CTC ACC CTG GAG AAG TTC ACG ATT CAC AAT TAT TCC CAC	880
Lys Thr Phe Leu Thr Leu Glu Lys Phe Thr Ile His Asn Tyr Ser His	
15 20 25	
TCC AGG GAG CGG CCG TAC AAG TGT GTG CAG CCT GAC TGT GGC AAA GCC	928
Ser Arg Glu Arg Pro Tyr Lys Cys Val Gln Pro Asp Cys Gly Lys Ala	
30 35 40	
TTT GTT TCC AGA TAT AAA TTG ATG AGG CAT ATG GCT ACC CAT TCT CCC	976
Phe Val Ser Arg Tyr Lys Leu Met Arg His Met Ala Thr His Ser Pro	
45 50 55	
CAG AAA TCT CAC CAG TGT GCT CAC TGT GAG AAG ACG TTC AAC CGG AAA	1024
Gln Lys Ser His Gln Cys Ala His Cys Glu Lys Thr Phe Asn Arg Lys	
60 65 70	
GAC CAC CTG AAA AAC CAC CTC CAG ACC CAC GAC CCC AAC AAA ATG GCC	1072
Asp His Leu Lys Asn His Leu Gln Thr His Asp Pro Asn Lys Met Ala	
75 80 85 90	
TTT GGG TGT GAG GAG TGT GGG AAG AAG TAC AAC ACC ATG CTG GGC TAT	1120
Phe Gly Cys Glu Glu Cys Gly Lys Lys Tyr Asn Thr Met Leu Gly Tyr	
95 100 105	
AAG AGG CAC CTG GCC CTC CAT GCG GCC AGC AGT GGG GAC CTC ACC TGT	1168
Lys Arg His Leu Ala Leu His Ala Ala Ser Ser Gly Asp Leu Thr Cys	
110 115 120	
GGG GTC TGT GCC CTG GAG CTA GGG AGC ACC GAG GTG CTA CTG GAC CAC	1216
Gly Val Cys Ala Leu Glu Leu Gly Ser Thr Glu Val Leu Leu Asp His	
125 130 135	
CTC AAA GCC CAT GCG GAA GAG AAG CCC CCT AGC GGA ACC AAG GAA AAG	1264
Leu Lys Ala His Ala Glu Glu Lys Pro Pro Ser Gly Thr Lys Glu Lys	
140 145 150	
AAG CAC CAG TGC GAC CAC TGT GAA AGA TGC TTC TAC ACC CGG AAG GAT	1312
Lys His Gln Cys Asp His Cys Glu Arg Cys Phe Tyr Thr Arg Lys Asp	
155 160 165 170	

GTG CGA CGC CAC CTG GTG GTC CAC ACA GGA TGC AAG GAC TTC CTG TGC Val Arg Arg His Leu Val Val His Thr Gly Cys Lys Asp Phe Leu Cys 175 180 185	1360
CAG TTC TGT GCC CAG AGA TTT GGG CGC AAG GAT CAC CTC ACC CGG CAT Gln Phe Cys Ala Gln Arg Phe Gly Arg Lys Asp His Leu Thr Arg His 190 195 200	1408
ACC AAG AAG ACC CAC TCA CAG GAG CTG ATG AAA GAG AGC TTG CAG ACC Thr Lys Lys Thr His Ser Gln Glu Leu Met Lys Glu Ser Leu Gln Thr 205 210 215	1456
GGA GAC CTT CTG AGC ACC TTC CAC ACC ATC TCG CCT TCA TTC CAA CTG Gly Asp Leu Leu Ser Thr Phe His Thr Ile Ser Pro Ser Phe Gln Leu 220 225 230	1504
AAG GCT GCT GCC TTG CCT CCT TTC CCT TTA GGA GCT TCT GCC CAG AAC Lys Ala Ala Ala Leu Pro Pro Phe Pro Leu Gly Ala Ser Ala Gln Asn 235 240 245 250	1552
GGG CTT GCA AGT AGC TTG CCA GCT GAG GTC CAT AGC CTC ACC CTC AGT Gly Leu Ala Ser Ser Leu Pro Ala Glu Val His Ser Leu Thr Leu Ser 255 260 265	1600
CCC CCA GAA CAA GCC GCC CAG CCT ATG CAG CCG CTG CCA GAG TCC CTG Pro Pro Glu Gln Ala Ala Gln Pro Met Gln Pro Leu Pro Glu Ser Leu 270 275 280	1648
GCC TCC CTC CAC CCC TCG GTA TCC CCT GGC TCT CCT CCG CCA CCC CTT Ala Ser Leu His Pro Ser Val Ser Pro Gly Ser Pro Pro Pro Pro Leu 285 290 295	1696
CCC AAT CAC AAG TAC AAC ACC ACT TCT ACC TCA TAC TCC CCA CTT GCA Pro Asn His Lys Tyr Asn Thr Thr Ser Thr Ser Tyr Ser Pro Leu Ala 300 305 310	1744
AGC CTG CCC CTC AAA GCA GAT ACT AAA GGT TTT TGC AAT ATC AGT TTG Ser Leu Pro Leu Lys Ala Asp Thr Lys Gly Phe Cys Asn Ile Ser Leu 315 320 325 330	1792
TTT GAG GAC TTG CCT CTG CAA GAG CCT CAG TCA CCT CAA AAG CTC AAC Phe Glu Asp Leu Pro Leu Gln Glu Pro Gln Ser Pro Gln Lys Leu Asn 335 340 345	1840
CCA GGT TTT GAT CTG GCT AAG GGA AAT GCT GGT AAA GTA AAC CTG CCC Pro Gly Phe Asp Leu Ala Lys Gly Asn Ala Gly Lys Val Asn Leu Pro 350 355 360	1888
AAG GAG CTG CCT GCA GAT GCT GTG AAC CTA ACA ATA CCT GCC TCT CTG Lys Glu Leu Pro Ala Asp Ala Val Asn Leu Thr Ile Pro Ala Ser Leu 365 370 375	1936
GAC CTG TCC CCC CTG TTG GGC TTC TGG CAG CTG CCC CCT CCT GCT ACC Asp Leu Ser Pro Leu Leu Gly Phe Trp Gln Leu Pro Pro Pro Ala Thr	1984



380	395	390	
CAA AAT ACC TTT GGG AAT AGC ACT CTT GCC CTG GGG CCT GGG GAA TCT			2032
Gln Asn Thr Phe Gly Asn Ser Thr Leu Ala Leu Gly Pro Gly Glu Ser			
395	400	405	410
TTG CCC CAC AGG TTA AGC TGT CTG GGG CAG CAG CAG CAA GAA CCC CCA			2080
Leu Pro His Arg Leu Ser Cys Leu Gly Gln Gln Gln Gln Glu Pro Pro			
	415	420	425
CTT GCC ATG GGC ACT GTG AGC CTG GGC CAG CTC CCC CTG CCC CCC ATC			2128
Leu Ala Met Gly Thr Val Ser Leu Gly Gln Leu Pro Leu Pro Pro Ile			
	430	435	440
CCT CAT GTG TTC TCA GCT GGC ACT GGC TCT GCC ATC CTG CCT CAT TTC			2176
Pro His Val Phe Ser Ala Gly Thr Gly Ser Ala Ile Leu Pro His Phe			
	445	450	455
CAT CAT GCA TTC AGA T AATTGATTTT TAAAGTGTAT TTTTCGTATT			2222
His His Ala Phe Arg			
	460		
CTGGAAGATG TTTTAAGAAG CATTTTAAAT GTCAGTACACA ATATGAGAAA GATTTGGAAA			2282
ACGAGACTGG GACTATGGCT TATTCAGTGA TGACTGGCTT GAGATGATAA GA			2334

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met	Ala	Thr	Phe	Pro	Cys	Gln	Leu	Cys	Gly	Lys	Thr	Phe	Leu	Thr	Leu
1				5					10				15		
Glu	Lys	Phe	Thr	Ile	His	Asn	Tyr	Ser	His	Ser	Arg	Glu	Arg	Pro	Tyr
			20					25					30		
Lys	Cys	Val	Gln	Pro	Asp	Cys	Gly	Lys	Ala	Phe	Val	Ser	Arg	Tyr	Lys
		35					40					45			
Leu	Met	Arg	His	Met	Ala	Thr	His	Ser	Pro	Gln	Lys	Ser	His	Gln	Cys
	50					55					60				
Ala	His	Cys	Glu	Lys	Thr	Phe	Asn	Arg	Lys	Asp	His	Leu	Lys	Asn	His
65					70				75					80	
Leu	Gln	Thr	His	Asp	Pro	Asn	Lys	Met	Ala	Phe	Gly	Cys	Glu	Glu	Cys
				85				90						95	

Gly Lys Lys Tyr Asn Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu  
 100 105 110

His Ala Ala Ser Ser Gly Asp Leu Thr Cys Gly Val Cys Ala Leu Glu  
 115 120 125

Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ala His Ala Glu  
 130 135 140

Glu Lys Pro Pro Ser Gly Thr Lys Glu Lys Lys His Gln Cys Asp His  
 145 150 155 160

Cys Glu Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val  
 165 170 175

Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg  
 180 185 190

Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His Ser  
 195 200 205

Gln Glu Leu Met Lys Glu Ser Leu Gln Thr Gly Asp Leu Leu Ser Thr  
 210 215 220

Phe His Thr Ile Ser Pro Ser Phe Gln Leu Lys Ala Ala Ala Leu Pro  
 225 230 235 240

Pro Phe Pro Leu Gly Ala Ser Ala Gln Asn Gly Leu Ala Ser Ser Leu  
 245 250 255

Pro Ala Glu Val His Ser Leu Thr Leu Ser Pro Pro Glu Gln Ala Ala  
 260 265 270

Gln Pro Met Gln Pro Leu Pro Glu Ser Leu Ala Ser Leu His Pro Ser  
 275 280 285

Val Ser Pro Gly Ser Pro Pro Pro Pro Leu Pro Asn His Lys Tyr Asn  
 290 295 300

Thr Thr Ser Thr Ser Tyr Ser Pro Leu Ala Ser Leu Pro Leu Lys Ala  
 305 310 315 320

Asp Thr Lys Gly Phe Cys Asn Ile Ser Leu Phe Glu Asp Leu Pro Leu  
 325 330 335

Gln Glu Pro Gln Ser Pro Gln Lys Leu Asn Pro Gly Phe Asp Leu Ala  
 340 345 350

Lys Gly Asn Ala Gly Lys Val Asn Leu Pro Lys Glu Leu Pro Ala Asp  
 355 360 365

Ala Val Asn Leu Thr Ile Pro Ala Ser Leu Asp Leu Ser Pro Leu Leu  
 370 375 380

Gly Phe Trp Gln Leu Pro Pro Pro Ala Thr Gln Asn Thr Phe Gly Asn  
385 390 395 400

Ser Thr Leu Ala Leu Gly Pro Gly Glu Ser Leu Pro His Arg Leu Ser  
405 410 415

Cys Leu Gly Gln Gln Gln Gln Glu Pro Pro Leu Ala Met Gly Thr Val  
420 425 430

Ser Leu Gly Gln Leu Pro Leu Pro Pro Ile Pro His Val Phe Ser Ala  
435 440 445

Gly Thr Gly Ser Ala Ile Leu Pro His Phe His His Ala Phe Arg  
450 455 460

B'

---



Dkt. 52130-A-PCT-US/JPW/EMW

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Dietmar Spengler and Laurent Journot  
Serial No. : 09/254,870 Examiner: C. Patterson  
Filed : August 16, 1999 Group Art Unit: 1652  
For : NUCLEIC ACID MOLECULES CODING FOR TUMOR  
SUPPRESSOR PROTEINS AND METHODS FOR THEIR  
ISOLATION

1185 Avenue of the Americas  
New York, New York 10036  
June 26, 2000

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the enclosed computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(f) has the same information which is submitted as the paper copy of the "Sequence Listing" attached hereto as **Exhibit B**.

Respectfully submitted,

Elizabeth M. Wieckowski  
Elizabeth M. Wieckowski  
Registration No. 42,226  
Cooper & Dunham LLP  
1185 Avenue of the Americas  
New York, New York 10036  
(212) 278-0400